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MIXED STOCK ANALYSIS OF JUVENILE HAWKSBILL FORAGING GROUNDS IN THE CARIBBEAN

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Mitochondrial DNA has proven useful for the elucidation of population structure and questions concerning the behavior of adult female hawksbills (*Eretmochelys imbricata*). In addition, a previous analysis of a juvenile foraging population at Mona Island, Puerto Rico, has provided information that more than one nesting location contributes individuals to a particular foraging site. What can the analysis of multiple disjunct foraging sites tell us about hawksbills? Investigations into the composition of juvenile foraging

grounds may provide insight into migration and behavior in hawksbills in the Caribbean. Are there differences in the genetic composition of different foraging locations? This paper will discuss the findings from the previous studies. In addition, multiple foraging locations in the eastern Caribbean have been sampled and the genetic composition of these sites has been determined. The potential causes (e.g. management practices or biotic factors) of differences in foraging ground composition at these locations are discussed.

POPULATION STRUCTURE, PHYLOGEOGRAPHY, AND MOLECULAR EVOLUTION

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Molecular genetic techniques have been applied to sea turtle biology for ten years, and substantial progress has been made on aspects of behavior, natural history, and evolution. Genetic results support the natal homing theory as a general paradigm for marine turtles, and have demonstrated the importance of continental barriers in shaping the intraspecific phylogeography of these species. Comparisons of nuclear and mitochondrial DNA illuminate aspects of reproductive biology, most especially the possibility of male-mediated gene flow between some nesting populations. DNA sequence comparisons in a phylogenetic context demonstrate an evolutionary separation of the ridley species, but do not support a species-level designation for *Chelonia*

agassizi. The application of rookery-specific genetic markers for tracing the migrations of marine turtles shows much promise. It is this approach that will most effectively serve the future needs wildlife management programs, as they begin to address the aquatic components of marine turtle natural history and conservation. However, government-sponsored management programs have a history of overutilization scientific tools (such as mechanical tags) and this would be very costly in the context of molecular assays. Studies which employ genetic markers must have a clearly-defined goal and end-point, and should not be used for ongoing monitoring except under special circumstances.

GENETIC STOCK IDENTIFICATION AND DISTRIBUTION OF LEATHERBACKS IN THE PACIFIC: POTENTIAL EFFECTS ON DECLINING POPULATIONS

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Analyses of mitochondrial DNA (mtDNA) control region sequence variation in combination with nuclear (NucDNA) data from 6 microsatellite loci indicate that eastern and western/Indo-Pacific nesting populations are genetically distinct and suggests these regional nesting assemblages represent independent demographic units for management purposes. To date, samples have been obtained from six leatherbacks caught in the Hawaii-based pelagic longline fishery. Four had haplotypes only found in the western/Indo-Pacific populations, while two had haplotypes only found in the eastern Pacific populations, indicating that both regional stocks are affected by this fishery in the north Pacific.

Additional samples obtained from strandings off the coasts of North America and South America confirm trans-

oceanic migrations by leatherbacks in the Pacific, and examination of the distribution of samples allows hypotheses to be drawn on the migratory patterns. The sudden and drastic decline of nesting populations in Mexico coincides with

the growing longline and coastal gillnet fisheries around the Pacific, and this study suggests that animals from eastern Pacific stocks migrate through areas both in the north Pacific and Southeast Pacific where these fisheries operate.

TENDENCY TOWARD SINGLE PATERNITY IN LEATHERBACKS DETECTED WITH MICROSATELLITES

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Molecular techniques provide new tools for peeking into the sex life of sea turtles. Observations on courtship and mating in leatherbacks are almost non-existent, although sea turtles are generally presumed to be promiscuous based on extensive studies of green turtles (Alvarado and Figueroa, 1991). FitzSimmons (1996) surprisingly found that multiple paternity was rare in Australian greens. Leatherback paternity studies to date have been invalid due to an insufficient number of reliable polymorphic loci. We have identified informative new microsatellite loci, and have sampled successive clutches laid by the same females over a three month period in St. Croix, U. S. Virgin Islands. A total of 6 loci were used to construct the genotypes of nesting females and their offspring. Loci were amplified by PCR using fluorescent dye-labelled primers analyzed on a 377A ABI automated sequencer with GENESCAN. Paternal genotypes were inferred by comparing the known offspring and known maternal genotypes. Using allele frequencies for the St. Croix nesting population, the probability of detecting multiple paternal alleles (d) was determined for each locus and across all loci (D) (see FitzSimmons, 1996). The probability of detecting multiple paternity was relatively low for some individual loci (DC99 and N32 in particular), combined D for all 6 loci was 99%. Analysis of data from a total of 178 hatchlings from series of 3 to 5 clutches (n=17 total) laid by each of 4 females, did not reveal any evidence of multiple paternity. Unexpected paternal alleles were detected in four cases; however, since in each case these alleles were only present at one locus, they were considered to be mutations rather than contributions by a second male. Two instances of mutation of the maternal allele were also detected

in this way. Mutation rates were highest in DC2-95, one of the most polymorphic loci. The lack of multiple paternity in this study corroborates previous findings with microsatellites for green turtles in Australia (FitzSimmons, 1996), and suggests either that female leatherbacks rarely mate with multiple males (perhaps as a result of behavioral factors, like competition, or because they rarely encounter them), or that sperm competition occurs. Either scenario would require the ability to store sperm. The detection of mutation within one generation turnover emphasizes the importance of using multiple loci when attempting to detect multiple paternity with microsatellites. Samples from additional females are presently being analyzed.

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CONTRIBUTION OF A NESTING COLONY OF HAWKSBILL TURTLE *ERETMOCHELYS IMBRICATA* TO SOME FEEDING GROUNDS IN CUBAN PLATFORM

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INTRODUCTION

Mitochondrial (mt) DNA genealogies have figured prominently in genetic studies of marine turtle, in spite of

typically exhibiting low rate of molecular evolution relative to many other organism groups (Bowen and Avise, 1995). Hawksbill turtles mt DNA have been useful in the definition